<!--StartFragment-->RESULT 5
AAM49641
ID   AAM49641 standard; protein; 836 AA.
XX
AC   AAM49641;
XX
DT   17-MAY-2002 (first entry)
XX
DE   Human tumour-associated antigen B345 protein SEQ ID NO 4.
XX
KW   Tumour-associated antigen; human; B345; cytostatic; cell communication;
KW   cell interaction; signal transduction; metastasis; cancer; colon;
KW   immunotherapy; carcinoma; lung; diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO200204508-A1.
XX
PD   17-JAN-2002.
XX
PF   05-JUL-2001; 2001WO-EP007705.
XX
PR   07-JUL-2000; 2000DE-01033080.
PR   19-APR-2001; 2001DE-01019294.
XX
PA   (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX
PI   Schweifer N, Scherl-Mostageer M, Sommergruber W, Abseher R;
XX
DR   WPI; 2002-171704/22.
DR   N-PSDB; ABA99507.
XX
PT   New tumor-associated antigen B345, useful for diagnosis and immunotherapy
PT   of tumors, also related nucleic acid and antibodies.
XX
PS   Claim 1; Page 85-88; 102pp; German.
XX
CC   This invention describes a novel tumour-associated antigen, designated
CC   B345 which has cytostatic activity. B345 is involved in communication,
CC   interaction and/or signal transduction with extracellular components and
CC   ligands, especially in the metastatic potential of cancers, particularly
CC   of the colon. B345 or its immunogenic fragments, also the DNA that
CC   encodes it, are useful for immunotherapy of cancer, particularly
CC   carcinoma of lung or colon. Antibodies raised against B345 are useful for
CC   treatment and diagnosis of cancers that are associated with B345
CC   expression, including their use for targeted delivery of cytotoxic or
CC   radioactive agents. Probes derived from B345 can be used to detect tumour
CC   -specific mutations in the B345 sequence, and can be used to screen for
CC   B345 specific modulators. This sequence represents a human B345 tumour-
CC   associated antigen described in the invention
XX
SQ   Sequence 836 AA;

  Query Match   99.8%; Score 4385; DB 5; Length 836;
  Best Local Similarity   99.8%; Pred. No. 0;
  Matches 834; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MAGLNCGVSIALLGVLLLGAARLPRGAEAFEIALPRESNITVLIKLGTPTLLAKPCYIVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MAGLNCGVSIALLGVLLLGAARLPRGAEAFEIALPRESNITVLIKLGTPTLLAKPCYIVI 60

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Qy          61 SKRHITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMSGPCPFGEVQLQPSTSLLPT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 SKRHITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMSGPCPFGEVQLQPSTSLLPT 120

Qy         121 LNRTFIWDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVTHSISGRIDATVVRIGTFCSN 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 LNRTFIWDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVTHSISGRIDATVVRIGTFCSN 180

Qy         181 GTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANY 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANY 240

Qy         241 PEGFPEDELMTWQFVVPAHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDK 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 PEGFPEDELMTWQFVVPAHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDK 300

Qy         301 QPGNMAGNFNLSLQGCDQDAQSPGILRLQFQVLVQHPQNESNKIYVVDLSNERAMSLTIE 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 QPGNMAGNFNLSLQGCDQDAQSPGILRLQFQVLVQHPQNESNKIYVVDLSNERAMSLTIE 360

Qy         361 PRPVKQSRKFVPGCFVCLESRTCSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDH 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 PRPVKQSRKFVPGCFVCLESRTCSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDH 420

Qy         421 RYCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKDRLSLVLVPAQKLQQHTHEKPCNTSF 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 RYCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKDRLSLVLVPAQKLQQHTHEKPCNTSF 480

Qy         481 SYLVASAIPSQDLYFGSFCPGGSIKQIQVKQNISVTLRTFAPSFRQEASRQGLTVSFIPY 540
               ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db         481 SYLVASAIPSQDLYFGSFCPGGSIKQIQVKQNISVTLRTFAPSFQQEASRQGLTVSFIPY 540

Qy         541 FKEEGVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLTFFKERSGVVCQ 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 FKEEGVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLTFFKERSGVVCQ 600

Qy         601 TGRAFMIIQEQRTRAEEIFSLDEDVLPKPSFHHHSFWVNISNCSPTSGKQLDLLFSVTLT 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 TGRAFMIIQEQRTRAEEIFSLDEDVLPKPSFHHHSFWVNISNCSPTSGKQLDLLFSVTLT 660

Qy         661 PRTVDLTVILIAAVGGGVLLLSALGLIICCVKKKKKKTNKGPAVGIYNGNINTEMPRQPK 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 PRTVDLTVILIAAVGGGVLLLSALGLIICCVKKKKKKTNKGPAVGIYNGNINTEMPRQPK 720

Qy         721 KFQKGRKDNDSHVYAVIEDTMVYGHLLQDSSGSFLQPEVDTYRPFQGTMGVCPPSPPTIC 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 KFQKGRKDNDSHVYAVIEDTMVYGHLLQDSSGSFLQPEVDTYRPFQGTMGVCPPSPPTIC 780

Qy         781 SRAPTAKLATEEPPPRSPPESESEPYTFSHPNNGDVSSKDTDIPLLSTQEPMEPAE 836
               ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db         781 SRAPTAKLATEEPPPRSPPESESEPYTFSHPNNGDVSSKDTDIPLLNTQEPMEPAE 836
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<!--EndFragment-->